



RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/572,027ADATE: 10/14/97  
TIME: 14:02:31

INPUT SET: S20979.raw

47 (A) APPLICATION NUMBER: US 07/575,542  
48 (B) FILING DATE: 30-AUG-1990  
49 (C) CLASSIFICATION:  
50  
51 (viii) ATTORNEY/AGENT INFORMATION:  
52 (A) NAME: Ellinger, Mark S.  
53 (B) REGISTRATION NUMBER: 34,812  
54 (C) REFERENCE/DOCKET NUMBER: A21-535.10  
55  
56 (ix) TELECOMMUNICATION INFORMATION:  
57 (A) TELEPHONE: 612/335-5070  
58 (B) TELEFAX: 612/288-9696  
59  
60 (2) INFORMATION FOR SEQ ID NO:1:  
61  
62 (i) SEQUENCE CHARACTERISTICS:  
63 (A) LENGTH: 1155 base pairs  
64 (B) TYPE: nucleic acid  
65 (C) STRANDEDNESS: single  
66 (D) TOPOLOGY: linear  
67  
68 (ii) MOLECULE TYPE: DNA  
69  
70 (iii) HYPOTHETICAL: NO  
71  
72 (iv) ANTI-SENSE: NO  
73  
74 (vi) ORIGINAL SOURCE:  
75 (A) ORGANISM: Brassica napus  
76  
77 (ix) FEATURE:  
78 (D) OTHER INFORMATION: Wild type F form.  
79  
80  
81 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
82  
83 ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT 48  
84 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser  
85 1 5 10 15  
86  
87 GAA ACC GAC ACC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT 96  
88 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr  
89 20 25 30  
90  
91 GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG 144  
92 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser  
93 35 40 \* 45  
94  
95 ATC CCT CGC TCT TTC TCC TAC CTC ATC~~T~~GAC ATC ATC ATA GCC TCC 192  
96 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ala Ser  
97 50 55 60  
98  
99 TGC TTC TAC TAC NTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT 240

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100	Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro			
101	65	70	75	80
102				
103	CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAA GGG TGC GTC			288
104	Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val			
105	85	90	95	
106				
107	CTA ACC GGC GTC TGG GTC ATA GCC CAC GAA TGC GGC CAC CAC GCC TTC			336
108	Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe			
109	100	105	110	
110				
111	AGC GAC TAC CAG TGG CTT GAC GAC ACC GTC GGT CTC ATC TTC CAC TCC			384
112	Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser			
113	115	120	125	
114				
115	TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGC AGC CAC			432
116	Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His			
117	130	135	140	
118				
119	CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG			480
120	His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys			
121	145	150	155	160
122				
123	AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG			528
124	Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu			
125	165	170	175	
126				
127	GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCG TTG			576
128	Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu			
129	180	185	190	
130				
131	TAC TTA GCC TTC AAC GTC TCG GGA AGA CCT TAC GAC GGC GGC TTC CGT			624
132	Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Arg			
133	195	200	205	
134				
135	TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC			672
136	Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu			
137	210	215	220	
138				
139	CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC TAC GGT CTC			720
140	Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu			
141	225	230	235	240
142				
143	TTC CGT TAC GCC GGC CAG GGA GTG GCC TCG ATG GTC TGC TTC TAC			768
144	Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr			
145	245	250	255	
146				
147	GGA GTC CCG CTT CTG ATT GTC AAT GGT TTC CTC GTG TTG ATC ACT TAC			816
148	Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr			
149	260	265	270	
150				
151	TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAC GAT TCG TCC GAG TGG			864
152	Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp			

**RAW SEQUENCE LISTING  
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153	275	280	285	
154				
155	GAT TGG TTC AGG GGA GCT TTG GCT ACC GTT GAC AGA GAC TAC GGA ATC			912
156	Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile			
157	290	295	300	
158				
159	TTG AAC AAG GTC TTC CAC AAT ATT ACC GAC ACG CAC GTG GCC CAT CAT			960
160	Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His			
161	305	310	315	320
162				
163	CCG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GCT ACC AAG GCG			1008
164	Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala			
165	325	330	335	
166				
167	ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG			1056
168	Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val			
169	340	345	350	
170				
171	GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG			1104
172	Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro			
173	355	360	365	
174				
175	GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T			1153
176	Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu			
177	370	375	380	
178				
179	GA			1155
180				
181				
182	(2) INFORMATION FOR SEQ ID NO:2:			
183				
184	(i) SEQUENCE CHARACTERISTICS:			
185	(A) LENGTH: 384 amino acids			
186	(B) TYPE: amino acid			
187	(D) TOPOLOGY: linear			
188				
189	(ii) MOLECULE TYPE: protein			
190				
191	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:			
192				
193	Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser			
194	1	5	10	15
195				
196	Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr			
197	20	25	30	
198				
199	Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser			
200	35	40	45	
201				
202	Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser			
203	50	55	60	
204				
205	Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro			

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206	65	70	75	80
207				
208	Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val			
209		85	90	95
210				
211	Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe			
212		100	105	110
213				
214	Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser			
215		115	120	125
216				
217	Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His			
218		130	135	140
219				
220	His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys			
221		145	150	155
222				160
223	Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu			
224		165	170	175
225				
226	Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu			
227		180	185	190
228				
229	Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg			
230		195	200	205
231				
232	Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu			
233		210	215	220
234				
235	Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu			
236		225	230	235
237				240
238	Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr			
239		245	250	255
240				
241	Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr			
242		260	265	270
243				
244	Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp			
245		275	280	285
246				
247	Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile			
248		290	295	300
249				
250	Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His			
251		305	310	315
252				320
253	Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala			
254		325	330	335
255				
256	Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val			
257		340	345	350
258				

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**SEQUENCE VERIFICATION REPORT**  
PATENT APPLICATION **US/08/572,027A**

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Original Text